

SUPPLEMENTARY MATERIAL

Supplementary Figures: Primer extension analysis of 7 mitochondrial RNAs from *Monoblepharella15*. The sequence reports the DNA sequencing ladder, which gives the reverse-complement of the sequences shown in Figure 3. Arrows indicate the location of the reverse transcriptase stops (bands containing the majority of the radioactively-labeled cDNA) from which RNA 5'-ends were inferred.

Supplementary Table

Codon usage in the mtDNAs of *H. curvatum*, *Harpochytrium94*, *Harpochytrium105* and *Monoblepharella15*

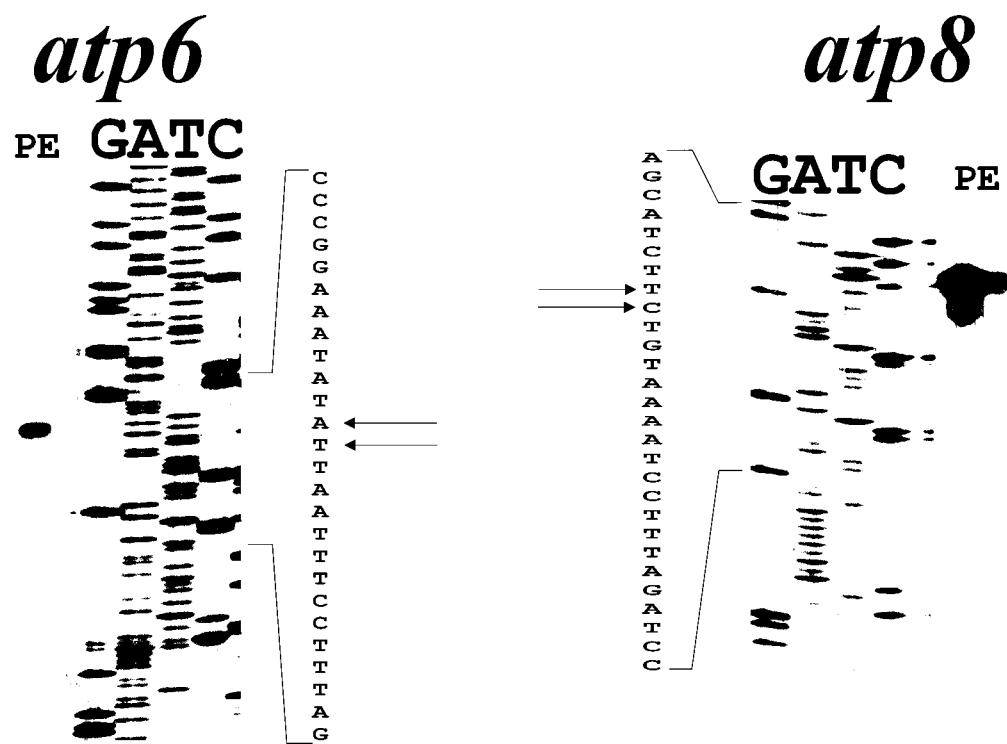
| a.a./codon ^a | total ^b | a.a./codon | total | a.a./codon | total | a.a./codon | total |
|-------------------------|------------------------|--------------|---------------------|--------------|-----------------------|--------------|-----------------------|
| F TTT | 103/127/162/137 | S TCT | 59/172/171/164 | Y TAT | 82/134/165/144 | C TGT | 1/12/14/14 |
| F TTC | 192/216/179/201 | S TCC | 55/16/17/11 | Y TAC | 101/56/32/53 | C TGC | 12/8/4/6 |
| L TTA | 56/344/343/329 | S TCA | 0/0/0/0 | * TAA | 13/13/12/13 | * TGA | 0/0/0/0 |
| L TTG | 76/1/1/1 | S TCG | 14/0/0/0 | * TAG | 1/1/2/1 | W TGG | 87/77/77/77 |
| L CTT | 187/318/318/308 | P CCT | 86/90/103/91 | H CAT | 25/47/65/61 | R CGT | 56/74/69/87 |
| L CTC | 175/29/30/24 | P CCC | 20/7/5/3 | H CAC | 66/43/26/37 | R CGC | 12/5/4/5 |
| L CTA | 86/2/3/8 | P CCA | 50/62/51/66 | Q CAA | 53/57/57/53 | R CGA | 26/9/8/2 |
| L CTG | 114/0/0/0 | P CCG | 11/3/4/7 | Q CAG | 20/0/0/0 | R CGG | 1/0/0/0 |
| I ATT | 187/295/304/287 | T ACT | 108/183/175/169 | N AAT | 37/53/77/70 | S AGT | 61/75/77/62 |
| I ATC | 92/22/17/45 | T ACC | 76/23/27/38 | N AAC | 72/65/40/51 | S AGC | 55/11/9/17 |
| I ATA | 0/0/0/3 | T ACA | 13/0/0/0 | K AAA | 45/58/58/57 | R AGA | 0/13/22/12 |
| M ATG | 182/142/142/144 | T ACG | 17/0/0/0 | K AAG | 9/0/0/0 | R AGG | 0/0/0/2 |
| V GTT | 82/195/194/215 | A GCT | 209/243/261/230 | D GAT | 42/79/89/73 | G GGT | 84/286/272/258 |
| V GTC | 84/30/11/29 | A GCC | 96/36/18/54 | D GAC | 49/21/13/28 | G GGC | 13/5/4/23 |
| V GTA | 72/42/63/28 | A GCA | 0/1/2/7 | E GAA | 51/72/71/75 | G GGA | 172/0/0/5 |
| V GTG | 56/2/4/3 | A GCG | 0/0/0/1 | E GAG | 27/0/0/0 | G GGG | 32/3/18/4 |

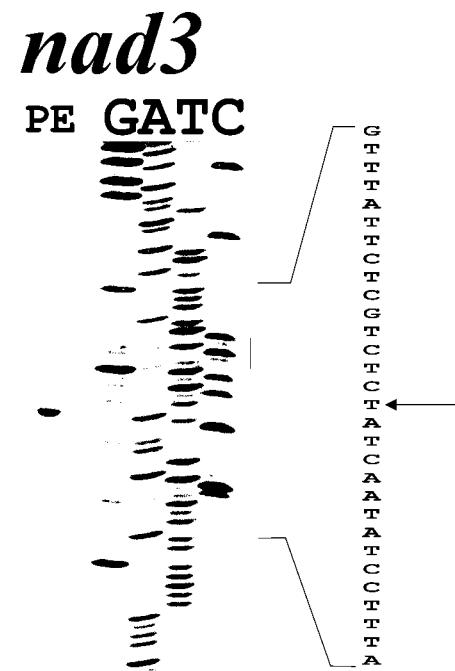
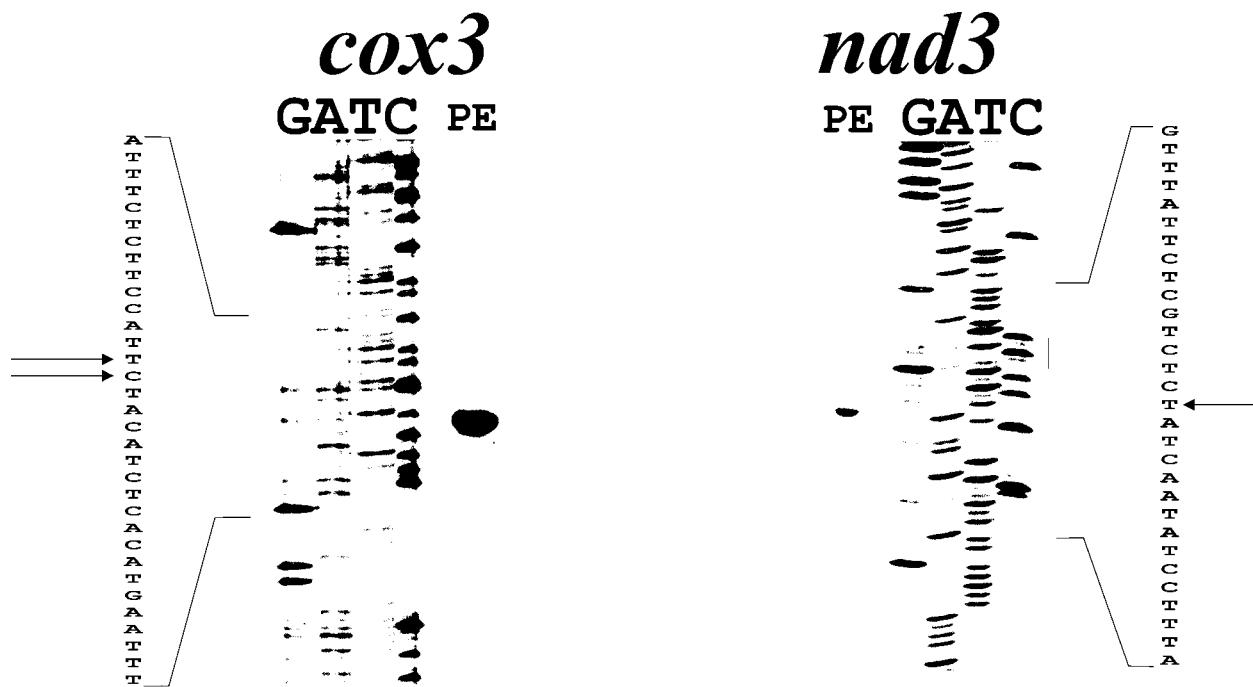
^aCognate amino acid (a.a.) is indicated in one-letter code. Asterix (*) indicates a stop codon. The correlation of amino acids and codons reflects the universal translation code, as inferred from the analysis of multiple protein alignments that did not reveal any deviations from the standard code.

^bNumbers indicate the total number of codons in the protein-coding genes (does not include intronic or free-standing ORFs) of *H. curvatum/Harpochytrium94/Harpochytrium105/Monoblepharella15*

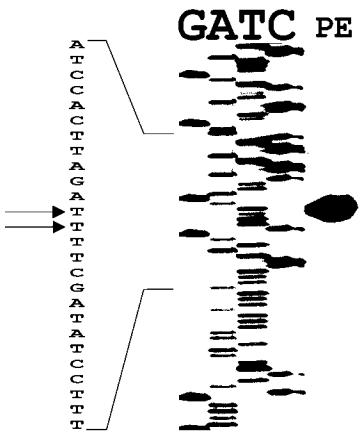
Bold indicates codons recognized by mtDNA-encoded tRNAs

Supplementary figures

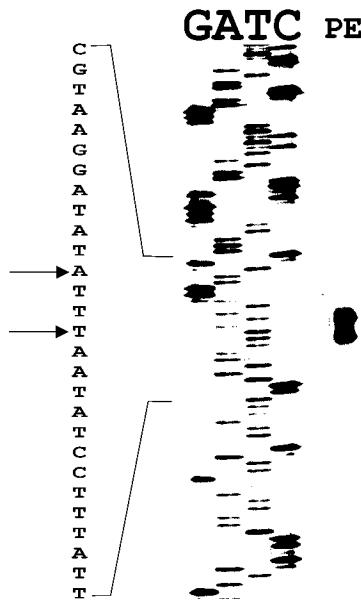




nad4L



nad5



nad6

